

# Hepatoprotective effects of systemic ER activation

Physiological parameters mice upon sacrifice

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25 July, 2023

```
# library import
library(ggplot2)
library(dplyr)

# color palettes
colPals <- list()
colPals$conditions <- setNames(c('#44AA99', '#117733', '#88CCFF', '#332288', '#DDCC77', '#CC6677', '#AA4499', '#882255'),
  c('CDf', 'HFDf', 'CDm', 'HFDm', 'DPN', 'DIP', 'E2', 'PPT'))
colPals$RdBu <- rev(RColorBrewer::brewer.pal(n=11, name = 'RdBu'))
colPals$UpDown <- setNames(colPals$RdBu[c(10,2)],
  c('up', 'down'))
```

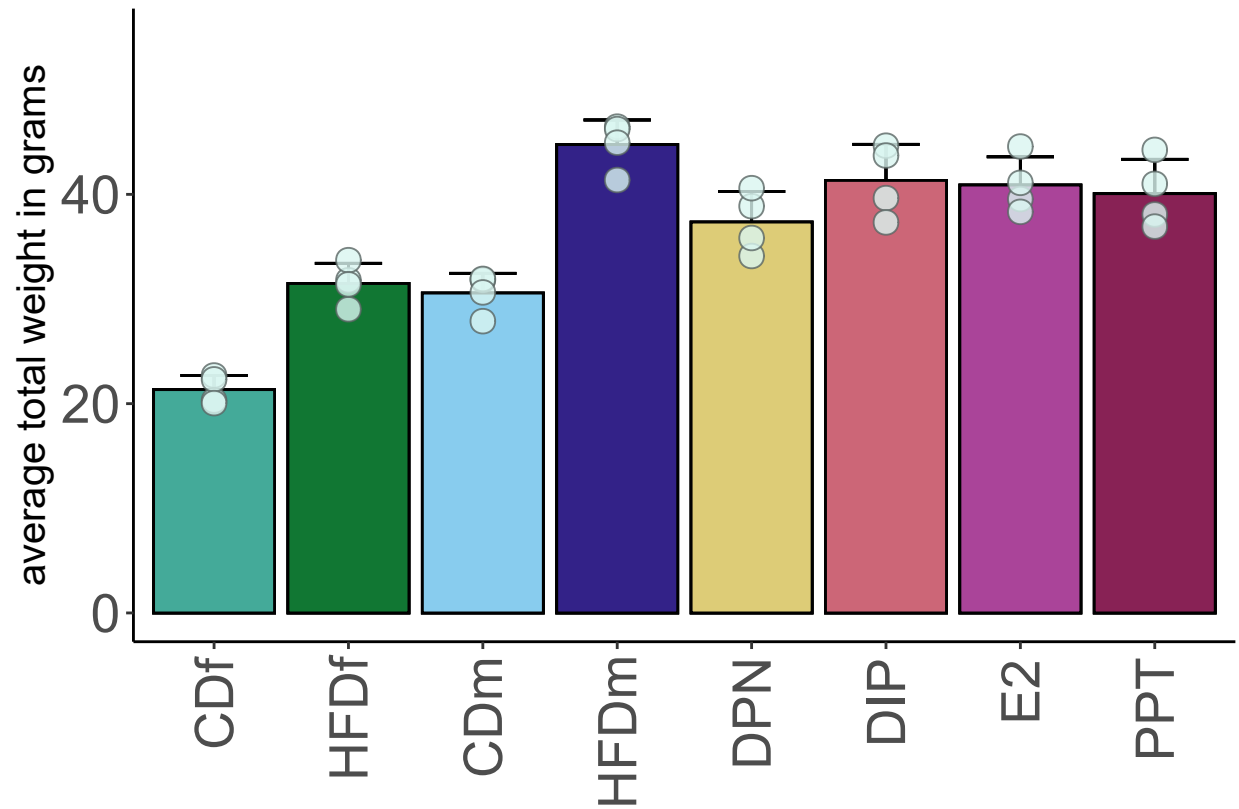
## Load data

```
phys_parameters <- read.delim("data/220923_physio_parameters.txt") %>%
  dplyr::mutate(group = gsub('_fe','f',group)) %>%
  dplyr::mutate(group = gsub('_ma','m',group)) %>%
  dplyr::mutate(group = factor(group, levels = names(colPals$conditions)))
```

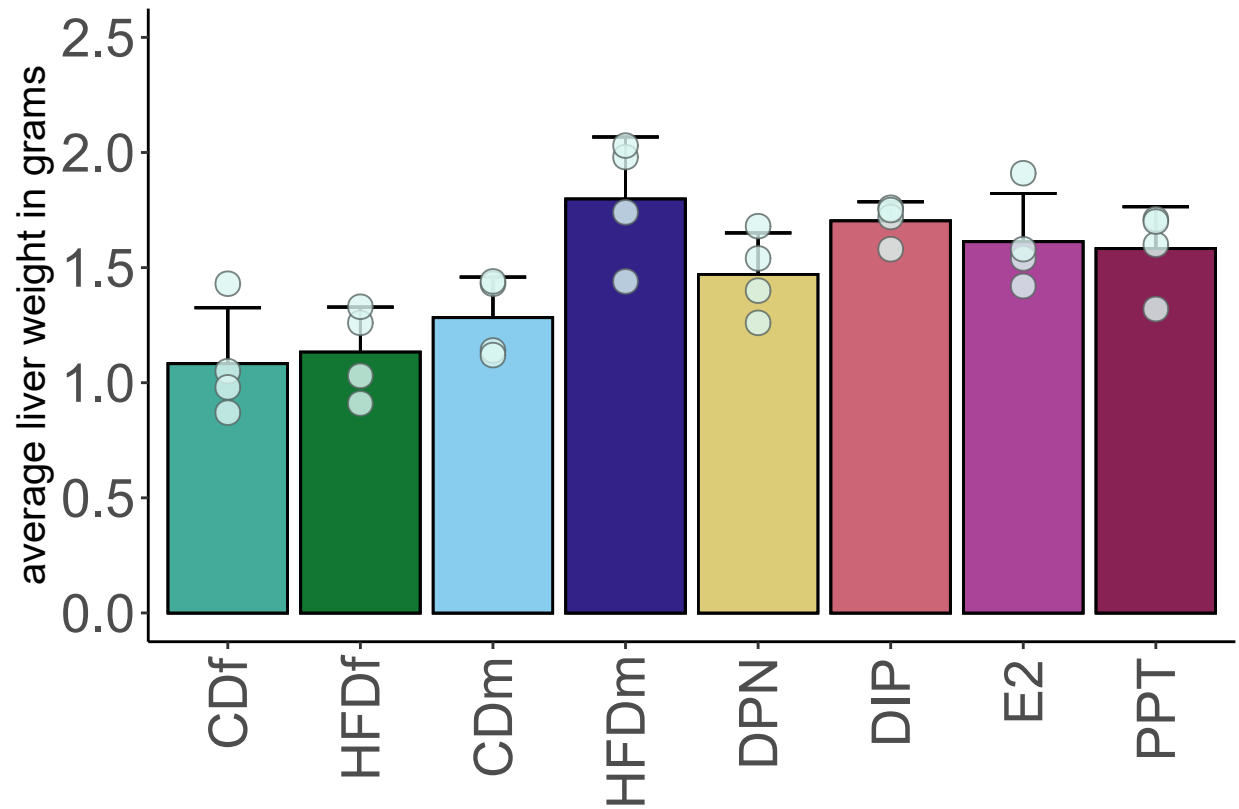
## Calculate means and standard deviations

```
phys_para_avg_sd <- phys_parameters %>%
  group_by(group) %>%
  mutate(liver_average = mean(liver)) %>%
  mutate(glucose_average = mean(glucose)) %>%
  mutate(tot_weight_average = mean(total_weight)) %>%
  mutate(liver_sd = sd(liver)) %>%
  mutate(glucose_sd = sd(glucose)) %>%
  mutate(tot_weight_sd = sd(total_weight))

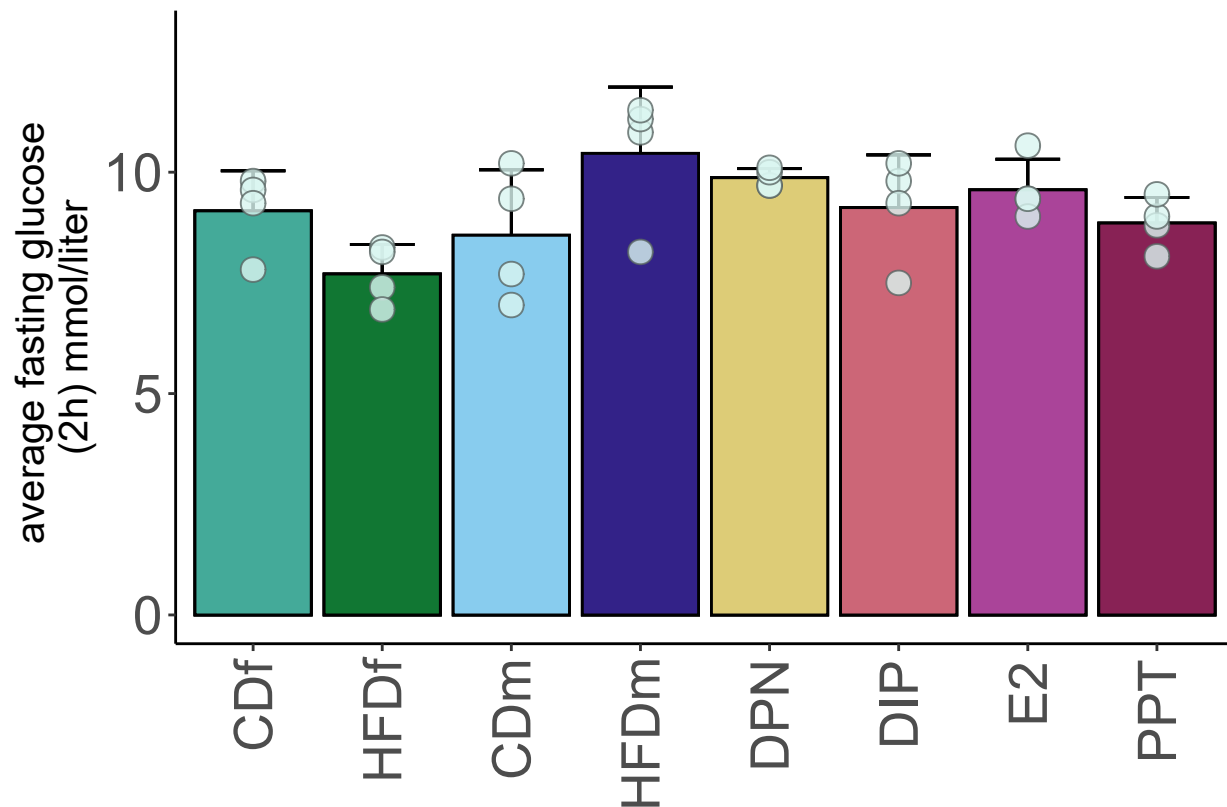
# Plot the total weight
ggplot(phys_para_avg_sd,
  aes(x=group,
    y = tot_weight_average)) +
  geom_errorbar(aes(ymin=tot_weight_average-tot_weight_sd,
    ymax=tot_weight_average+tot_weight_sd),
    width = 0.5, color="black") +
  geom_col(aes(fill=group), position= "dodge", color="black") +
  geom_point(aes(y = total_weight), shape=21, size=4, color="#5a6664", fill="#daf6f1", alpha=0.8) +
  theme_bw() +
  theme_classic()+
  theme(axis.text.x = element_text(angle=90, size = 20, vjust = 0.5, hjust = 0.95),
    axis.text.y = element_text(size = 20),
    axis.title.y = element_text(size = 15),
    legend.position = "none") +
  scale_y_continuous(limits = c(0, 55)) +
  scale_fill_manual(values = colPals$condition) +
  xlab("") +
  ylab("average total weight in grams")
```



```
# Plot the liver weight
ggplot(phys_para_avg_sd,
  aes(x=group,
    y = liver_average)) +
  geom_errorbar(aes(ymin=liver_average-liver_sd,
    ymax=liver_average+liver_sd),
    width = 0.5, color="black") +
  geom_col(aes(fill=group), position= "dodge", color="black") +
  geom_point(aes(y = liver),shape=21,size=4, color="#5a6664", fill="#daf6f1", alpha=0.8) +
  theme_bw() +
  theme_classic()+
  theme(axis.text.x = element_text(angle=90, size = 20, vjust = 0.5, hjust = 0.95),
    axis.text.y = element_text(size = 20),
    axis.title.y = element_text(size = 15),
    legend.position = "none") +
  scale_y_continuous(limits = c(0, 2.5)) +
  scale_fill_manual(values = colPals$condition) +
  xlab("") +
  ylab("average liver weight in grams")
```



```
# Plot the blood glucose 2h before sacrifice
ggplot(phys_para_avg_sd,
  aes(x=group,
    y = glucose_average)) +
  geom_errorbar(aes(ymin=glucose_average-glucose_sd,
    ymax=glucose_average+glucose_sd,
    width = 0.5, color="black")) +
  geom_col(aes(fill=group), position= "dodge", color="black") +
  geom_point(aes(y = glucose),shape=21,size=4, color="#5a6664", fill="#daf6f1", alpha=0.8) +
  theme_bw() +
  theme_classic()+
  theme(axis.text.x = element_text(angle=90, size = 20, vjust = 0.5, hjust = 0.95),
    axis.text.y = element_text(size = 20),
    axis.title.y = element_text(size = 15),
    legend.position = "none") +
  scale_y_continuous(limits = c(0, 13)) +
  scale_fill_manual(values = colPals$condition) +
  xlab("") +
  ylab("average fasting glucose \n(2h) mmol/liter")
```



## Perform statistical tests

```
total <- aov(phys_parameters$total_weight ~ phys_parameters$group)
TukeyHSD(total)

## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = phys_parameters$total_weight ~ phys_parameters$group)
##
## $`phys_parameters$group`
##      diff      lwr      upr    p adj
## HFDf-CDf 10.1400  4.1054574 16.174543 0.0002339
## CDm-CDf   9.2250  3.1904574 15.259543 0.0007993
## HFDm-CDf 23.4150 17.3804574 29.449543 0.0000000
## DPN-CDf  16.0100  9.9754574 22.044543 0.0000001
## DIP-CDf  19.9900 13.9554574 26.024543 0.0000000
## E2-CDf   19.5475 13.5129574 25.582043 0.0000000
## PPT-CDf  18.7250 12.6904574 24.759543 0.0000000
## CDm-HFDf -0.9150 -6.9495426  5.119543 0.9995399
## HFDm-HFDf 13.2750  7.2404574 19.309543 0.0000040
## DPN-HFDf  5.8700 -0.1645426 11.904543 0.0606528
## DIP-HFDf  9.8500  3.8154574 15.884543 0.0003450
## E2-HFDf   9.4075  3.3729574 15.442043 0.0006253
## PPT-HFDf  8.5850  2.5504574 14.619543 0.0018883
## HFDm-CDm 14.1900  8.1554574 20.224543 0.0000013
## DPN-CDm   6.7850  0.7504574 12.819543 0.0199440
## DIP-CDm  10.7650  4.7304574 16.799543 0.0001016
## E2-CDm   10.3225  4.2879574 16.357043 0.0001832
## PPT-CDm   9.5000  3.4654574 15.534543 0.0005522
## DPN-HFDm -7.4050 -13.4395426 -1.370457 0.0090084
## DIP-HFDm -3.4250 -9.4595426  2.609543 0.5763689
## E2-HFDm  -3.8675 -9.9020426  2.167043 0.4294434
## PPT-HFDm -4.6900 -10.7245426  1.344543 0.2136604
## DIP-DPN   3.9800 -2.0545426 10.014543 0.3946359
## E2-DPN    3.5375 -2.4970426  9.572043 0.5380364
```

```
## PPT-DPN      2.7150   -3.3195426   8.749543  0.8051408
## E2-DIP      -0.4425   -6.4770426   5.592043  0.9999966
## PPT-DIP     -1.2650   -7.2995426   4.769543  0.9963820
## PPT-E2      -0.8225   -6.8570426   5.212043  0.9997720

liver <- aov(phys_parameters$liver ~ phys_parameters$group)
TukeyHSD(liver)

## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = phys_parameters$liver ~ phys_parameters$group)
##
## $`phys_parameters$group`
##      diff      lwr      upr      p adj
## HFDf-CDf  0.0500 -0.41703769 0.5170377 0.9999548
## CDm-CDf    0.2000 -0.26703769 0.6670377 0.8401374
## HFDm-CDf   0.7150  0.24796231 1.1820377 0.0007850
## DPN-CDf    0.3875 -0.07953769 0.8545377 0.1562704
## DIP-CDf    0.6200  0.15296231 1.0870377 0.0040610
## E2-CDf     0.5300  0.06296231 0.9970377 0.0184176
## PPT-CDf    0.5000  0.03296231 0.9670377 0.0298835
## CDm-HFDf   0.1500 -0.31703769 0.6170377 0.9584177
## HFDm-HFDf  0.6650  0.19796231 1.1320377 0.0018697
## DPN-HFDf   0.3375 -0.12953769 0.8045377 0.2886268
## DIP-HFDf   0.5700  0.10296231 1.0370377 0.0094904
## E2-HFDf    0.4800  0.01296231 0.9470377 0.0409360
## PPT-HFDf   0.4500 -0.01703769 0.9170377 0.0646912
## HFDm-CDm   0.5150  0.04796231 0.9820377 0.0234987
## DPN-CDm    0.1875 -0.27953769 0.6545377 0.8785182
## DIP-CDm    0.4200 -0.04703769 0.8870377 0.1001372
## E2-CDm     0.3300 -0.13703769 0.7970377 0.3137170
## PPT-CDm    0.3000 -0.16703769 0.7670377 0.4266819
## DPN-HFDm   -0.3275 -0.79453769 0.1395377 0.3223779
## DIP-HFDm   -0.0950 -0.56203769 0.3720377 0.9969960
## E2-HFDm    -0.1850 -0.65203769 0.2820377 0.8855085
## PPT-HFDm   -0.2150 -0.68203769 0.2520377 0.7871701
## DIP-DPN    0.2325 -0.23453769 0.6995377 0.7177056
## E2-DPN     0.1425 -0.32453769 0.6095377 0.9682535
## PPT-DPN    0.1125 -0.35453769 0.5795377 0.9916298
## E2-DIP     -0.0900 -0.55703769 0.3770377 0.9978562
## PPT-DIP    -0.1200 -0.58703769 0.3470377 0.9877977
## PPT-E2     -0.0300 -0.49703769 0.4370377 0.9999986

glucose <- aov(phys_parameters$glucose ~ phys_parameters$group)
TukeyHSD(glucose)
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = phys_parameters$glucose ~ phys_parameters$group)
##
## $`phys_parameters$group`
##      diff      lwr      upr      p adj
## HFDf-CDf  -1.425 -3.7639468 0.9139468 0.4913448
## CDm-CDf   -0.550 -2.8889468 1.7889468 0.9927438
## HFDm-CDf   1.300 -1.0389468 3.6389468 0.6006337
## DPN-CDf    0.750 -1.5889468 3.0889468 0.9587631
## DIP-CDf    0.075 -2.2639468 2.4139468 1.0000000
## E2-CDf     0.475 -1.8639468 2.8139468 0.9970258
## PPT-CDf   -0.275 -2.6139468 2.0639468 0.9999150
## CDm-HFDf   0.875 -1.4639468 3.2139468 0.9117560
## HFDm-HFDf  2.725  0.3860532 5.0639468 0.0146030
## DPN-HFDf   2.175 -0.1639468 4.5139468 0.0815407
## DIP-HFDf   1.500 -0.8389468 3.8389468 0.4286430
## E2-HFDf    1.900 -0.4389468 4.2389468 0.1737124
## PPT-HFDf   1.150 -1.1889468 3.4889468 0.7295532
## HFDm-CDm   1.850 -0.4889468 4.1889468 0.1972545
## DPN-CDm    1.300 -1.0389468 3.6389468 0.6006337
## DIP-CDm    0.625 -1.7139468 2.9639468 0.9847248
## E2-CDm     1.025 -1.3139468 3.3639468 0.8244024
## PPT-CDm    0.275 -2.0639468 2.6139468 0.9999150
## DPN-HFDm   -0.550 -2.8889468 1.7889468 0.9927438
## DIP-HFDm   -1.225 -3.5639468 1.1139468 0.6662725
## E2-HFDm    -0.825 -3.1639468 1.5139468 0.9333570
## PPT-HFDm   -1.575 -3.9139468 0.7639468 0.3697376
## DIP-DPN    -0.675 -3.0139468 1.6639468 0.9765162
## E2-DPN     -0.275 -2.6139468 2.0639468 0.9999150
## PPT-DPN    -1.025 -3.3639468 1.3139468 0.8244024
## E2-DIP     0.400 -1.9389468 2.7389468 0.9989959
## PPT-DIP    -0.350 -2.6889468 1.9889468 0.9995780
```

```
## PPT-E2      -0.750 -3.0889468 1.5889468 0.9587631
```

## SessionInfo

```
sessionInfo()
```

```
## R version 4.0.5 (2021-03-31)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 19045)
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=English_United States.1252
## [2] LC_CTYPE=English_United States.1252
## [3] LC_MONETARY=English_United States.1252
## [4] LC_NUMERIC=C
## [5] LC_TIME=English_United States.1252
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] dplyr_1.1.2  ggplot2_3.3.3
##
## loaded via a namespace (and not attached):
## [1] highr_0.10      pillar_1.9.0    compiler_4.0.5  RColorBrewer_1.1-3
## [5] tools_4.0.5     digest_0.6.27   evaluate_0.21   lifecycle_1.0.3
## [9] tibble_3.2.1    gtable_0.3.3    pkgconfig_2.0.3  rlang_1.1.1
## [13] cli_3.6.1       rstudioapi_0.13  yaml_2.2.1      xfun_0.31
## [17] fastmap_1.1.0   withr_2.5.0     stringr_1.4.0   knitr_1.31
## [21] generics_0.1.3  vctrs_0.6.3     grid_4.0.5      tidyselect_1.2.0
## [25] glue_1.4.2      R6_2.5.1        fansi_0.4.2     rmarkdown_2.14
## [29] farver_2.0.3    magrittr_2.0.3   scales_1.2.1    htmltools_0.5.2
## [33] colorspace_2.0-0 labeling_0.4.2   utf8_1.1.4      stringi_1.5.3
## [37] munsell_0.5.0
```